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Whole-Genome Sequence of *Starmerella bacillaris* PAS13, a Nonconventional Enological Yeast with Antifungal Activity

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ABSTRACT *Starmerella bacillaris* is a fermentative yeast commonly found in vineyards. Here, we present the draft genome sequence of *S. bacillaris* PAS13, a nonconventional enological yeast with a potential role as a biocontrol agent. This gene sequence will provide insights into the genetic basis of yeast activity against gray mold disease (*Botrytis cinerea*).

To reduce the use of pesticides, biocontrol agents have been developed as potential alternatives to agrochemicals in integrated crop management (1). They can be a relevant part of an effective strategy to improve sustainable agricultural systems. In this context, several nonconventional yeasts, such as *Candida intermedia*, *Sporidiobolus pararoseus*, *Saccharomyces cerevisiae* (*Sa. cerevisiae*), and *Starmerella bacillaris* (*St. bacillaris*) (formerly *Candida zemplinina*) have been studied, given their ability to produce volatile organic compounds endowed with biocontrol activity against *Botrytis cinerea*. Moreover, *St. bacillaris* activity against gray mold has also been demonstrated *in vivo* on grape berries (2, 3). Furthermore, wine cofermentations (sequential or mixed inoculum) using *St. bacillaris* and *Sa. cerevisiae* have been widely investigated in recent years. These fermentations were characterized by the complementary consumption of glucose (by *Sa. cerevisiae*) and fructose (by *St. bacillaris*) with a consequent increase in glycerol and succinic acid contents, which is associated with low ethanol and acetoin production. This is an interesting feature for the improvement of wine quality and the reduction of ethanol content in wine (4–6).

St. bacillaris is commonly found in enological environments (7). Here, we present the draft genome sequence of *St. bacillaris* PAS13, isolated from destemmed dried grapes of the Raboso Piave variety, cultivated in the Bagnoli DOC (Guaranteed Origin Name) area in northeast Italy.

For genomic DNA extraction, zymolyase digestion followed by standard phenol-chloroform purification, as described by Vaughan-Martini and Martini (8), was used. Illumina 1-kb mate-paired libraries were prepared at the Ramaciotti Centre for Genomics (Sydney, Australia) and run on an Illumina NextSeq 500 platform. The sequencing resulted in a 147-fold genome coverage using 9,651,388 high-quality paired-end (2 × 150-bp) and unpaired reads. The *de novo* assembly was performed using SPAdes version 3.10 (with option -k 21,33,55,77,99,127) (9), generating a draft genome of 9.4 Mb with a GC content of 39.45%. The high quality of the assembly was proved by the presence of only 67 contigs in the genome (*N*₅₀ length of 318,510 bp). GeneMark-ES software was used for predicting protein-coding sequences (CDSs) (10), and the results indicated the presence of 4,321 CDSs and 4,322 exons. According to Lemos Junior et al.

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(11), two different approaches were used for gene annotation, namely, BlastKOALA (12) and RPS BLAST. The first approach used members of the *Saccharomycetaceae* family as the taxonomy group to generate a nonredundant set of KEGG genes. The second approach was used to compare protein sequences with eukaryotic orthologous groups of proteins (KOG) (13). The *St. bacillaris* PAS13 genome reported here will help in understanding the metabolism of this yeast and its potential role as a biocontrol agent in vineyards.

Accession number(s). The whole-genome shotgun project of *St. bacillaris* PAS13 has been deposited in DDBJ/ENA/GenBank under the accession no. [MWPI000000000](https://www.ncbi.nlm.nih.gov/nuccore/MWPI000000000). The version described in this paper is the first version, MWPI01000000.

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REFERENCES

- Bai Z, Jin B, Li Y, Chen J, Li Z. 2008. Utilization of winery wastes for *Trichoderma viride* biocontrol agent production by solid state fermentation. *J Environ Sci* 20:353–358. [https://doi.org/10.1016/S1001-0742\(08\)60055-8](https://doi.org/10.1016/S1001-0742(08)60055-8).
- Belda I, Ruiz J, Alonso A, Marquina D, Santos A. 2017. The biology of *Pichia membranifaciens* killer toxins. *Toxins* 9:112. <https://doi.org/10.3390/toxins9040112>.
- Lemos Junior WJF, Bovo B, Nadai C, Crosato G, Carlot M, Favaron F, Giacomini A, Corich V. 2016. Corrigendum: biocontrol ability and action mechanism of *Starmerella bacillaris* (synonym *Candida zemplinina*) isolated from wine musts against gray mold disease agent *Botrytis cinerea* on grape and their effects on alcoholic fermentation. *Front Microbiol* 7:1249. <https://doi.org/10.3389/fmicb.2016.01499>.
- Rantsiou K, Dolci P, Giacosa S, Torchio F, Tofalo R, Torriani S, Suzzi G, Rolle L, Cocolin L. 2012. *Candida zemplinina* can reduce acetic acid produced by *Saccharomyces cerevisiae* in sweet wine fermentations. *Appl Environ Microbiol* 78:1987–1994. <https://doi.org/10.1128/AEM.06768-11>.
- Englezos V, Rantsiou K, Torchio F, Rolle L, Gerbi V, Cocolin L. 2015. Exploitation of the non-*Saccharomyces* yeast *Starmerella bacillaris* (synonym *Candida zemplinina*) in wine fermentation: physiological and molecular characterizations. *Int J Food Microbiol* 199:33–40. <https://doi.org/10.1016/j.ijfoodmicro.2015.01.009>.
- Bovo B, Fontana F, Giacomini A, Corich V. 2011. Effects of yeast inoculation on volatile compound production by grape marcs. *Ann Microbiol* 61:117–124. <https://doi.org/10.1007/s13213-010-0106-4>.
- Bovo B, Giacomini A, Corich V. 2011. Effects of grape marcs acidification treatment on the evolution of indigenous yeast populations during the production of grappa. *J Appl Microbiol* 111:382–388. <https://doi.org/10.1111/j.1365-2672.2011.05060.x>.
- Vaughan-Martini A, Martini A. 1996. Isolation, purification, and analysis of nuclear DNA in yeast taxonomy. *Methods Mol Biol* 53:89–102. <https://doi.org/10.1385/0-89603-319-8:89>.
- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol* 19:455–477. <https://doi.org/10.1089/cmb.2012.0021>.
- Ter-Hovhannisyan V, Lomsadze A, Chernoff YO, Borodovsky M. 2008. Gene prediction in novel fungal genomes using an *ab initio* algorithm with unsupervised training. *Genome Res* 18:1979–1990. <https://doi.org/10.1101/gr.081612.108>.
- Lemos Junior WJF, Treu L, da Silva Duarte V, Campanaro S, Nadai C, Giacomini A, Coricha V. 2017. Draft genome sequence of the yeast *Starmerella bacillaris* (syn., *Candida zemplinina*) FRI751 isolated from fermenting must of dried raboso grapes. *Genome Announc* 5(17): e00224-17. <https://doi.org/10.1128/genomeA.00224-17>.
- Kanehisa M, Sato Y, Morishima K. 2016. BlastKOALA and GhostKOALA: KEGG tools for functional characterization of genome and metagenome sequences. *J Mol Biol* 428:726–731. <https://doi.org/10.1016/j.jmb.2015.11.006>.
- Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA. 2003. The COG database: an updated version includes eukaryotes. *BMC Bioinformatics* 4:41. <https://doi.org/10.1186/1471-2105-4-41>.